

SEQUENCE LISTING



<110> Pecker, Iris  
Vlodavsky , Israel  
Feinstein, Elena

<120> POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY AND EXPRESSION OF SAME  
IN GENETICALLY MODIFIED CELLS

<130> 27674

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<170> PatentIn version 3.1

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<213> Homo sapiens

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cacctccttg ccgagttcca gagcttcggg aggggtgggt acacttcagt attacattca 2340
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&lt;210&gt; 44

&lt;211&gt; 535

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 44

Met Leu Arg Leu Leu Leu Trp Leu Trp Gly Pro Leu Gly Ala Leu  
 1 5 10 15

Ala Gln Gly Ala Pro Ala Gly Thr Ala Pro Thr Asp Asp Val Val Asp  
 20 25 30

Leu Glu Phe Tyr Thr Lys Arg Pro Leu Arg Ser Val Ser Pro Ser Phe  
 35 40 45

Leu Ser Ile Thr Ile Asp Ala Ser Leu Ala Thr Asp Pro Arg Phe Leu  
 50 55 60

Thr Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu Ala Arg Gly Leu Ser  
 65 70 75 80

Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe  
 85 90 95

Asp Pro Asp Lys Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Lys Ser  
 100 105 110

Gln Val Asn His Asp Ile Cys Arg Ser Glu Pro Val Ser Ala Ala Val  
 115 120 125

Leu Arg Lys Leu Gln Val Glu Trp Pro Phe Gln Glu Leu Leu Leu  
 130 135 140

Arg Glu Gln Tyr Gln Lys Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser  
 145 150 155 160

Ser Val Asp Met Leu Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu  
 165 170 175

Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn  
 180 185 190

Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr  
 195 200 205

Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Trp Lys Lys  
 210 215 220

Ala His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu  
 225 230 235 240

Leu His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu Tyr  
 245 250 255

Gly Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu Leu Arg  
 260 265 270

Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Leu Thr Trp His  
275 280 285

His Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu Asp Phe Leu Ser  
290 295 300

Ser Asp Ala Leu Asp Thr Phe Ile Leu Ser Val Gln Lys Ile Leu Lys  
305 310 315 320

Val Thr Lys Glu Ile Thr Pro Gly Lys Lys Val Trp Leu Gly Glu Thr  
325 330 335

Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asn Thr Phe Ala  
340 345 350

Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala Gln Met Gly  
355 360 365

Ile Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His  
370 375 380

Leu Val Asp Glu Asn Phe Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu  
385 390 395 400

Leu Phe Lys Lys Leu Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys  
405 410 415

Gly Pro Asp Arg Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val  
420 425 430

Tyr His Pro Arg Tyr Gln Glu Gly Asp Leu Thr Leu Tyr Val Leu Asn  
435 440 445

Leu His Asn Val Thr Lys His Leu Lys Val Pro Pro Pro Leu Phe Arg  
450 455 460

Lys Pro Val Asp Thr Tyr Leu Leu Lys Pro Ser Gly Pro Asp Gly Leu  
465 470 475 480

Leu Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val Asp  
485 490 495

Glu Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala Gly Ser  
500 505 510

Ala Leu Ser Leu Pro Ala Phe Ser Tyr Gly Phe Phe Val Ile Arg Asn  
515 520 525

Ala Lys Ile Ala Ala Cys Ile  
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<210> 45

<211> 2396

<212> DNA

<213> Mus musculus

<220>



&lt;221&gt; CDS

&lt;222&gt; (594)..(2198)

&lt;223&gt;

&lt;400&gt; 45

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ttaaggcaga agggagtcgg ggtagggtct ggctgaaccc tcaaccgggg cttttaactc      180
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accaggaagc tgggtcccacc cctgcgcggc tcccgggcgc tccctcccca ggcctccgag      300
gatcttggtat tctggccacc tccgcaccct ttggatgggt gtggatgatt tcaaaagtgg      360
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cggggagggg agggcgctag ggagggaactc ccgggagggg tgggagggat ggagcgctgt      480
gggaggggtac tgagtcctgg cgccagaggc gaagcaggac cggttcagag gggcttgagc      540
cagcgcgccc gctgcccag ctctcccggc agcgggcggg ccagccagggt ggg atg      596
                                   Met
                                   1

ctg agg ctg ctg ctg ctg tgg ctc tgg ggg ccg ctc ggt gcc ctg gcc      644
Leu Arg Leu Leu Leu Trp Leu Trp Gly Pro Leu Gly Ala Leu Ala
                                   5                10                15

cag ggc gcc ccc gcg ggg acc gcg ccg acc gac gac gtg gta gac ttg      692
Gln Gly Ala Pro Ala Gly Thr Ala Pro Thr Asp Asp Val Val Asp Leu
                                   20                25                30

gag ttt tac acc aag ccg ccg ctc cga agc gtg agt ccc tcg ttc ctg      740
Glu Phe Tyr Thr Lys Arg Pro Leu Arg Ser Val Ser Pro Ser Phe Leu
                                   35                40                45

tcc atc acc atc gac gcc agc ctg gcc acc gac ccg cgc ttc ctc acc      788
Ser Ile Thr Ile Asp Ala Ser Leu Ala Thr Asp Pro Arg Phe Leu Thr
                                   50                55                60                65

ttc ctg ggc tct cca agg ctc cgt gct ctg gct aga ggc tta tct cct      836
Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu Ala Arg Gly Leu Ser Pro
                                   70                75                80

gca tac ttg aga ttt ggc ggc aca aag act gac ttc ctt att ttt gat      884
Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp
                                   85                90                95

ccg gac aag gaa ccg act tcc gaa gaa aga agt tac tgg aaa tct caa      932
Pro Asp Lys Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Lys Ser Gln
                                   100               105               110

gtc aac cat gat att tgc agg tct gag ccg gtc tct gct gcg gtg ttg      980
Val Asn His Asp Ile Cys Arg Ser Glu Pro Val Ser Ala Ala Val Leu
                                   115               120               125

agg aaa ctc cag gtg gaa tgg ccc ttc cag gag ctg ttg ctg ctc cga      1028
Arg Lys Leu Gln Val Glu Trp Pro Phe Gln Glu Leu Leu Leu Leu Arg
                                   130               135               140               145

gag cag tac caa aag gag ttc aag aac agc acc tac tca aga agc tca      1076
Glu Gln Tyr Gln Lys Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser
                                   150               155               160

gtg gac atg ctc tac agt ttt gcc aag tgc tcg ggg tta gac ctg atc      1124
Val Asp Met Leu Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu Ile
                                   165               170               175

ttt ggt cta aat gcg tta cta cga acc cca gac tta cgg tgg aac agc      1172
Phe Gly Leu Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn Ser
                                   180               185               190

tcc aac gcc cag ctt ctc ctt gac tac tgc tct tcc aag ggt tat aac      1220
Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn
                                   195               200               205

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atc tcc tgg gaa ctg ggc aat gag ccc aac agt ttc tgg aag aaa gct Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Trp Lys Lys Ala 210 215 220 225	1268
cac att ctc atc gat ggg ttg cag tta gga gaa gac ttt gtg gag ttg His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu Leu 230 235 240	1316
cat aaa ctt cta caa agg tca gct ttc caa aat gca aaa ctc tat ggt His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu Tyr Gly 245 250 255	1364
cct gac atc ggt cag cct cga ggg aag aca gtt aaa ctg ctg agg agt Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu Leu Arg Ser 260 265 270	1412
ttc ctg aag gct ggc gga gaa gtg atc gac tct ctt aca tgg cat cac Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Leu Thr Trp His His 275 280 285	1460
tat tac ttg aat gga cgc atc gct acc aaa gaa gat ttt ctg agc tct Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu Asp Phe Leu Ser Ser 290 295 300 305	1508
gat gcg ctg gac act ttt att ctc tct gtg caa aaa att ctg aag gtc Asp Ala Leu Asp Thr Phe Ile Leu Ser Val Gln Lys Ile Leu Lys Val 310 315 320	1556
act aaa gag atc aca cct ggc aag aag gtc tgg ttg gga gag acg agc Thr Lys Glu Ile Thr Pro Gly Lys Lys Val Trp Leu Gly Glu Thr Ser 325 330 335	1604
tca gct tac ggt ggc ggt gca ccc ttg ctg tcc aac acc ttt gca gct Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asn Thr Phe Ala Ala 340 345 350	1652
ggc ttt atg tgg ctg gat aaa ttg ggc ctg tca gcc cag atg ggc ata Gly Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala Gln Met Gly Ile 355 360 365	1700
gaa gtc gtg atg agg cag gtg ttc ttc gga gca ggc aac tac cac tta Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His Leu 370 375 380 385	1748
gtg gat gaa aac ttt gag cct tta cct gat tac tgg ctc tct ctt ctg Val Asp Glu Asn Phe Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu 390 395 400	1796
ttc aag aaa ctg gta ggt ccc agg gtg tta ctg tca aga gtg aaa ggc Phe Lys Lys Leu Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys Gly 405 410 415	1844
cca gac agg agc aaa ctc cga gtg tat ctc cac tgc act aac gtc tat Pro Asp Arg Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val Tyr 420 425 430	1892
cac cca cga tat cag gaa gga gat cta act ctg tat gtc ctg aac ctc His Pro Arg Tyr Gln Glu Gly Asp Leu Thr Leu Tyr Val Leu Asn Leu 435 440 445	1940
cat aat gtc acc aag cac ttg aag gta ccg cct ccg ttg ttc agg aaa His Asn Val Thr Lys His Leu Lys Val Pro Pro Pro Leu Phe Arg Lys 450 455 460 465	1988
cca gtg gat acg tac ctt ctg aag cct tcg ggg ccg gat gga tta ctt Pro Val Asp Thr Tyr Leu Leu Lys Pro Ser Gly Pro Asp Gly Leu Leu 470 475 480	2036
tcc aaa tct gtc caa ctg aac ggt caa att ctg aag atg gtg gat gag Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val Asp Glu 485 490 495	2084
cag acc ctg cca gct ttg aca gaa aaa cct ctc ccc gca gga agt gca Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala Gly Ser Ala 500 505 510	2132
cta agc ctg cct gcc ttt tcc tat ggt ttt ttt gtc ata aga aat gcc Leu Ser Leu Pro Ala Phe Ser Tyr Gly Phe Phe Val Ile Arg Asn Ala 515 520 525	2180
aaa atc gct gct tgt ata tgaaaaataaa aggcatacgg taccocctgag	2228

Lys Ile Ala Ala Cys Ile  
530 535

acaaaagccg aggggggtgt tattcataaa aaaaaaccct agtttaggag gccacctcct 2288  
tgccgagttc cagagcttcg ggagggtggg gtacacttca gtattacatt cagtgtggtg 2348  
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<211> 385

<212> DNA

<213> Rattus norvegicus

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caaagcgtga gtccctcgtt cctgtccatc accatcgacg ccagtctggc caccgacct 180  
cggttcctca ctttcctgag ctctccacgg cttcgagccc tgtctagagg cttatctcct 240  
gcgtacttga gatttggcgg caccaagact gacttcctta tttttgatcc caacaacgaa 300  
cccacctctg aagaaagaag ttactggcaa tctcaagaca acaatgatat ttgcgggtct 360  
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<210> 47

<211> 541

<212> DNA

<213> Rattus norvegicus

<220>

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<222> (507)..(507)

<223> Any nucleotide

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cattaactgt caccacctgc agtgggtctac ttagagaaca ccgactgga tgtaaacact 180  
gaagcgcgtg ccccgccctc ccgaggctct ggatccagcg ttgaagcttg ccccgccctc 240  
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aaggagtccg ctccctaccg ctggggtttt gctttattct tatgaatgac acccctgacc 360  
gctttcgtct cagggttact gtaatgcctt ttattttcat atacaagctg cgattttggc 420  
attttctatg acaaaaaacc cataggaaaa ggcgggcacg cttagtgcgc ttcctgcggg 480  
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<210> 48

<211> 126

<212> PRT

<213> Rattus norvegicus

&lt;400&gt; 48

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Thr Pro Ala Gly Thr Ala Pro Thr Lys Asp Val Val Asp Leu Glu Phe  
 20 25 30

Tyr Thr Lys Arg Leu Phe Gln Ser Val Ser Pro Ser Phe Leu Ser Ile  
 35 40 45

Thr Ile Asp Ala Ser Leu Ala Thr Asp Pro Arg Phe Leu Thr Phe Leu  
 50 55 60

Ser Ser Pro Arg Leu Arg Ala Leu Ser Arg Gly Leu Ser Pro Ala Tyr  
 65 70 75 80

Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Asn  
 85 90 95

Asn Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Gln Ser Gln Asp Asn  
 100 105 110

Asn Asp Ile Cys Gly Ser Asp Arg Val Ser Ala Asp Val Leu  
 115 120 125

&lt;210&gt; 49

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (9)..(9)

&lt;223&gt; Xaa can be any naturally occurring amino acid

&lt;400&gt; 49

Leu Lys Met Val Asp Glu Gln Thr Xaa Pro Ala Leu Thr Glu Lys Pro  
 1 5 10 15

Leu Pro Ala Gly Ser Ser Leu Ser Val Pro Ala Phe Ser Tyr Gly Phe  
 20 25 30

Phe Val Ile Arg Asn Ala Lys Ile Ala Ala Cys Ile  
 35 40